

GenCore version 5.1.4.p5.4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2003, 15:07:49 ; Search time 16.7601 Seconds  
(without alignments)  
1537.035 Million cell updates/sec

Title: US-08-978-217-7  
Perfect score: 445  
Sequence: 1 NCALBELRLVFGPLGDLHA.....ELLDGQQAAPYHPSGAG 84

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Xgapop 6.0 , Xgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues  
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPRO.spool/US08978217/runat\_14032003\_141838\_13457/app\_query.fasta\_1.1500  
-DB=issued\_Patents\_NA -QPM=faetac -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=0 -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTPMT=0 -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-NO\_XLPRY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELPE=6 -DELEXT=7

Database :

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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	100.0	1920	1	US-08-746-789A-1
2	72	16.2	521	4	US-09-404-879A-139
3	72	16.2	551	4	US-09-404-879A-92
4	72	16.2	555	4	US-09-404-879A-107
5	72	16.2	2301	1	US-08-306-691B-23
6	72	16.2	2301	5	PCT-US93-06251-78
7	71.5	16.1	3141	2	US-08-956-242-1
8	71.5	16.1	3141	3	US-09-351-215-1
9	66.5	14.9	1473	4	US-09-518-914-7
10	66	14.8	1594	2	US-08-955-713-1
11	66	14.8	4154	1	US-08-131-365B-37
12	66	14.8	4154	2	US-08-668-123-37

C 13	65.5	14.7	111282	4	US-09-754-250-3	Sequence 3, Appl1
14	64.5	14.5	3546	1	US-08-162-809-9	Sequence 9, Appl1
15	64.5	14.5	3591	1	US-08-162-809-13	Sequence 11, Appl1
C 16	64.5	14.5	3807	1	US-08-357-598-1	Sequence 1, Appl1
C 17	64.5	14.5	3807	2	US-09-003-289-1	Sequence 1, Appl1
C 18	64.5	14.5	3807	5	PCT-US95-16435-1	Sequence 1, Appl1
19	64	14.4	32207	4	US-08-770-379-20	Sequence 20, Appl1
20	64	14.4	32207	2	US-08-757-659A-20	Sequence 20, Appl1
21	64	14.4	32207	4	US-09-230-371A-20	Sequence 20, Appl1
22	63.5	14.3	1575	4	US-09-134-001C-516	Sequence 516, App
23	63.5	14.3	3103	4	US-09-268-480-10	Sequence 10, Appl1
C 24	63	14.2	9997	1	US-08-246-982A-15	Sequence 15, Appl1
C 25	63	14.2	9997	1	US-08-453-265-15	Sequence 15, Appl1
C 26	63	14.2	10103	2	US-08-457-273B-7	Sequence 7, Appl1
C 27	62	13.9	3469	2	US-09-221-017B-106	Sequence 106, App
C 28	62	13.9	3854	2	US-08-720-484A-1	Sequence 1, Appl1
C 29	62	13.9	3854	3	US-08-953-823A-1	Sequence 1, Appl1
C 30	62	13.9	3854	4	US-09-398-239-1	Sequence 1, Appl1
C 31	62	13.9	6256	2	US-08-475-891A-1	Sequence 1, Appl1
C 32	62	13.9	6256	2	US-08-567-375-1	Sequence 1, Appl1
C 33	62	13.9	6256	2	US-08-587-680A-1	Sequence 1, Appl1
C 34	62	13.9	1263	4	US-08-961-527-198	Sequence 198, App
35	61.5	13.8	2464	4	US-08-811-481-21	Sequence 21, Appl1
36	61.5	13.8	2943	2	US-08-548-159-2	Sequence 2, Appl1
37	61.5	13.8	2994	2	US-08-548-159-4	Sequence 2, Appl1
38	61.5	13.8	3777	3	US-09-121-321-15	Sequence 15, Appl1
39	61.5	13.8	3777	4	US-08-933-803A-15	Sequence 15, Appl1
40	61.5	13.8	5319	2	US-08-861-464-7	Sequence 7, Appl1
41	61.5	13.8	5319	2	US-08-396-001-7	Sequence 7, Appl1
42	61.5	13.8	5319	4	US-09-323-433A-7	Sequence 7, Appl1
43	61.5	13.8	477	2	US-08-465-380-35	Sequence 35, Appl1
C 44	61	13.7	477	2	US-08-486-397-35	Sequence 35, Appl1
C 45	61	13.7	477	2	US-08-486-397-35	Sequence 35, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-746-789A-1  
Sequence 1, Application US/08746789A  
Patent No. 5789200  
GENERAL INFORMATION:  
APPLICANT: Ismail Kola, Martin J. Tyms, Christine DeBuck  
TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELF3  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road, P.O. Box 1539  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/746,789A  
FILING DATE: No. 5789200ember 15, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: William T. Han  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: ATG 50024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610 270 5219  
TELEFAX: 610 270 4026  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:



QY 81 CysglyAla 83  
 Db 70 TGCCTTCA 62

## RESULT 4

US-09-404-879A-107/C  
 ; Sequence 107, Application US/09404879A  
 ; Patent No. 6468546  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: King, Gordon E.  
 ; APPLICANT: Aigate, Paul A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.462C2  
 ; CURRENT APPLICATION NUMBER: US/09/404, 879A  
 ; CURRENT FILING DATE: 1999-09-24  
 ; NUMBER OF SEQ ID NOS: 393  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 107  
 ; LENGTH: 555  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-09-404-879A-107

## Alignment Scores:

Pred. No.:	0-502	Length:	555
Score:	72.00	Matches:	31
Percent Similarity:	39.81%	Conservative:	10
Best Local Similarity:	30.10%	Mismatches:	32
Query Match:	16.18%	Indels:	31
DB:	4	Gaps:	5

US-08-978-217-7 (1-84) x US-09-404-879A-107 (1-555)

QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22  
 Db 358 GAGTTCATCTTTTCTTCATCTTTTAAGCCCGGTTTCAATACCTTCACTACCTCTCTC 299  
 QY 23 ArgAspLeuThrSerSerSerSerSerAspGluLeuSerTrpIleIleGluLeuLeuGly 42  
 Db 298 ACTCTCATCTACACAGCTTTTTCAGC-----TTCTTCACAGCTTTTTCAGGCGC 254  
 QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54  
 Db 253 AGTGCCACAGGCGCTCTGAGCAGGCTCCTTCTTCAACAGCTGATCTTACGGTT 194  
 QY 55 -----ProPheAspGlnGlySerProPheAlaGlnGluLeuLeu 67  
 Db 193 CAAGGAGGCACTCAGCTCAGCTGTTCCGGGCGCGCTTTCCT-CAACTTCTC 135  
 QY 68 AspAspGlyGlnGlnAlaSerProTyrrHis-----ProGlySer 80  
 Db 134 GCTGAGGCGCTCAGCTGCTCTCTGATCATCTGCTGCTGAGAACTGGATCT 75  
 QY 81 CysglyAla 83  
 Db 74 TGCCTTCA 66

## RESULT 5

US-08-306-691B-23/C  
 ; Sequence 23, Application US/08306691B  
 ; Patent No. 5734039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Calabretta, Bruno  
 ; APPLICANT: Skorski, Tomasz  
 ; TITLE OF INVENTION: ANTISENSE  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
 ; NUMBER OF SEQUENCES: 55  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
 ; STREET: Two Penn Center, Suite 1800

CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/306, 691B  
 FILING DATE: September 15, 1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monaco, Daniel A.  
 REGISTRATION NUMBER: 30,480  
 REFERENCE/DOCKET NUMBER: 8321-8  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-8383  
 TELEFAX: (215) 568-5549  
 TELEX: No. 5734039e  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2301 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 US-08-306-691B-23

## Alignment Scores:

Pred. No.:	3-39	Length:	2301
Score:	72.00	Matches:	31
Percent Similarity:	39.81%	Conservative:	10
Best Local Similarity:	30.10%	Mismatches:	32
Query Match:	16.18%	Indels:	31
DB:	1	Gaps:	5

US-08-978-217-7 (1-84) x US-08-306-691B-23 (1-2301)

QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22  
 Db 553 GAGTTCATCTTTTCTTCATCTTTTAAGCCCGGTTTCAATACCTTCACTACCTCTCTC 494  
 QY 23 ArgAspLeuThrSerSerSerSerSerAspGluLeuSerTrpIleIleGluLeuLeuGly 42  
 Db 493 ACTCTCATCTACACAGCTTTTTCAGC-----TTCTTCACAGCTTTTTCAGGCGC 449  
 QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54  
 Db 448 AGTGCCACAGGCGCTCTGAGCAGGCTCCTTCTTCAACAGCTGATCTTACGGTT 389  
 QY 55 -----ProPheAspGlnGlySerProPheAlaGlnGluLeuLeu 67  
 Db 388 CAAGGAGGCACTCAGCTCAGCTGTTCCGGGCGCGCTTTCCT-CAACTTCTC 330  
 QY 68 AspAspGlyGlnGlnAlaSerProTyrrHis-----ProGlySer 80  
 Db 329 GCTGAGGCGCTCAGCTGCTCTCTGATCATCTGCTGCTGAGAACTGGATCT 270  
 QY 81 CysglyAla 83  
 Db 269 TGCCTTCA 261

## RESULT 6

PCT-US93-06251-78/C  
 ; Sequence 78, Application PC/TUS9306251  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
 ; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
 ; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

```

NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT-US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 2301 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-78

Alignment Scores:
Pred. No.: 3.39 Length: 2301
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
DB: 5 Gaps: 5

US-08-978-217-7 (1-84) x PCT-US93-06251-78 (1-2301)
QY 6 GluleuArGleuValAlphe-----GlyProLeuGlYAspGlnLeuHIsAlaGlnLeu 22
||| ||| ||| ||| ||| :| | :| | :| | |||
Db 553 GAGTTCACATCTTTCTTCATCTTTTAAGGCCCGGTTTCAATAACCTTCADACTCTC 494
QY 23 ArgAspleuthrSerSerSerSerSerAspIleuSerTrpIleileGluLeuGlnLys 42
||||| :| | :| | :| | :| | :| | :| | :| |
Db 493 ACTCTCATCACACAGCTTTTTCAGC-----TTCTTCACAGCTTTTGACAGGC 449
QY 43 AspGlyMetAla-----PheGlnGluAlaLeuAspProGly--- 54
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 AGTGCCACGAGGGCTTCGTGACACGGCTCAGCTTTTCAACACAGCTGGATCTTAGCGTT 389
QY 55 -----ProPheAspGlnLysSerProphealaglnGluLeu 67
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 CAAGAGGCGCACCTCAGCGCTCAGCGCTGTTCCGGGCGCGCTTCTCCCT-CAACTCTC 330
QY 68 AspaAspGlyGlnGlnAlaSerProTyHis-----ProGlySer 80
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Db 329 GCTGAAGCGCTCAAGCTCGTCTCTGCTGATCATCTGCTGCTGAGAACCTGATCT 270
QY 81 CyeGlyAla 83
||| ||| :| | :| | :| | :| | :| | |||
Db 269 TGCGCTCA 261

RESULT 7
US-08-956-242-1
Sequence 1, Application US/08956242C
Patent No. 5986081
GENERAL INFORMATION:
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: APPLICANT: Ganetzky, Barry S.
: TITLE OF INVENTION: Polynucleotides Encoding Herg-3
: FILE REFERENCE: 960296.94550
: CURRENT APPLICATION NUMBER: US/08/956.242C
: CURRENT FILING DATE: 1997-10-22
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3141
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (248)..(2128)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (3)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (12)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1568)..(1872)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (3126)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (3134)
: OTHER INFORMATION: Unidentified at time of filing
: US-08-956-242-1
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: Alignment Scores:
: Pred. No.: 6.03 Length: 3141
: Score: 71.50 Matches: 37
: Percent Similarity: 37.17% Conservative: 5
: Best Local Similarity: 32.74% Mismatches: 28
: Query Match: 16.07% Indels: 44
: DB: 2 Gaps: 5
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: QY 9 LeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSer 28
: Db 2227 CTGAAGCTGGGGCTCCAGGCTAGAGCAAGCTCCAGCCCAAGATGACAGGCTGGAGTCCCGC 2286
:
: QY 29 SerSerAspGlnLeuSerTrpIleIleGlnLeuLeuGlnLys-----AspGlyMet 45
: Db 2287 GTGTCTTCAGACCTCAGCCGACCTTGAGCTCTTCAGAAAGCCAGTGCACCGAGGCCAC 2346
:
: QY 46 Ala-----PheGln 48
: Db 2347 GCCAGCTACATTCTGGAAGCCCTGCTCCAAATGACTGCTGGCTTGTTCTATTAGCTCG 2406
:
: QY 49 GlnAlaLeuAspProGlyPro----- 55
: Db 2407 GAGACAGACAGAGTCCAGGCGCCAGGCTGCCCAAGGGCTTTCGTCTTCGACAGACCCCA 2466
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: QY 56 -----PheAspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGln 71
: Db 2467 AGCTATGAGAGCTTGATGACTGTAGTCCAAA-GCACAGAACTCCTCC-----CAG 2519
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: QY 72 GlnAlaSerProGlyTrhisProGlySerCysGlyAlaGly 84
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Db 2520 GATGCTCACCT-----GGGTGGCAGACGA 2546

RESULT 8
US-09-351-215-1
: Sequence 1, Application US/09351215
: Patent No. 6087488
: GENERAL INFORMATION:
: APPLICANT: Ganetzky, Barry S.
: APPLICANT: Titus, Steven A.
: TITLE OF INVENTION: Polynucleotides Encoding Herg-3
: FILE REFERENCE: 960296..94550
: CURRENT APPLICATION NUMBER: US/09/351,215
: CURRENT FILING DATE: 1999-07-12
: EARLIER APPLICATION NUMBER: 08/956,242
: EARLIER FILING DATE: 1997-10-22
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3141
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (248)..(2126)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (3)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (12)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1568)..(1872)
: OTHER INFORMATION: Unidentified at time of filing
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (3126)
: OTHER INFORMATION: Unidentified at time of filing
: NAME/KEY: unsure
: LOCATION: (3134)
: OTHER INFORMATION: Unidentified at time of filing
US-09-351-215-1

Alignment Scores:
Pred. No.: 6.03 Length: 3141
Score: 71.50 Matches: 37
Percent Similarity: 37.17% Conservative: 5
Best Local Similarity: 32.74% Mismatches: 28
Query Match: 16.07% Indels: 44
DB: 3 Gaps: 5

US-08-978-217-7 (1-64) x US-09-351-215-1 (1-3141)
QY 9 LeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSer 28
Db 2227 CTGAAGCTGGAGCTCCAGAGCTAAGAGAGCTCCAGAGCCCAATGACATGACCTGGCTTGTCTATTACCTCG 2286
QY 29 SerSerArgGluLeuSerTPrIleIleGlnLeuLeuGlnLys-----AspGlyMet 45
Db 2287 GTGTCTCGAGCTCAAGCTCAAGCGCATCTTGAGACTCTCCAGAAAGCCATGCCCCAGAGGCGAC 2346
QY 46 Ala-----PheGln 48
Db 2347 GCCAGCTACATTCTGAAAGCCCTGCTCCATATGACTGCTGGCTTGTCTATTACCTCG 2406
QY 49 GluAlaLeuAspProGlyPro----- 55

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Db 2407 GAGACGACGAGTCCAGGGGCCCAAGCTGCCCCCAAGGGCTTTCTGCTTCTGACACAGACCCCA 2466
||| ||||| ||||| |||||
Oy 56 -----PheAspGlnGlySerProPheAlaGlnGluLeuAspAspGlyGln 71
||| ||||| ||||| ||||| |||||
Db 2467 AGCTATGAGACTGTGGATGACTGTAAGTCCAAA-GCAGAGAACTCCTCC-----CAG 2519
||| ||||| ||||| ||||| |||||
Oy 72 GlnAlaSerProGlyThrHisProGlySerGlyGlyAlaGly 84
||| ||||| ||||| ||||| |||||
Db 2520 GATGCTCCTCACT-----GGCTGTGGCAACGGA 2546
||| ||||| ||||| ||||| |||||

RESULT 9
US-09-518-914-7
; Sequence 7, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhlani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPM
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-518-914-7

Predicted Scores:
Pred. No.: 10.4 Length: 1473
Score: 66.50 Matches: 26
Percent Similarity: 36.84% Conservative: 9
Best Local Similarity: 27.37% Mismatches: 31
Query Match: 14.94% Indels: 29
DB: 4 Gaps: 4

US-08-978-217-7 (1-84) x US-09-518-914-7 (1-1473)
Oy 7 LeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeu----- 22
||| ||||| ||||| ||||| |||||
Db 1117 CTTGGGGTGGCTCTTGTGAGATGATGAGCCAGCGAGCACCCTCCTAGACGACTCT 1176
||| ||||| ||||| ||||| |||||
Oy 23 -----ArgAspLeuThrSerSerSerSerAspAspGluLeuSerTyrIleGlnLeuLeu 40
||| ||||| ||||| ||||| |||||
Db 1177 ACCCATGCTGCCACATGACGACACCGACGCTCCTGAGACTCAGCTGATC----- 1224
||| ||||| ||||| ||||| |||||
Oy 41 GluIysAspGlyMetAlaPheGlnGluAlaLeu-----AspProGlyProPhe 56
||| ||||| ||||| ||||| |||||
Db 1225 -----TCTGGGCAAGAGCCGCAAGAGTCCCTGGCTTCTGAGATGAAAGGGCTGGACA 1278
||| ||||| ||||| ||||| |||||
Oy 57 Asp-----GlnGlySerProPheAla 63
||| ||||| ||||| ||||| |||||
Db 1279 GACACAGAAACACACAGCTGCTGGGGAGCTGCCCAAGCAAGAGGACATCCTTCTGC 1338
||| ||||| ||||| ||||| |||||
Oy 64 GlnGluLeuLeuAspAspGlyGlnGlnAlaSerProGlyThrHisPro 78
||| ||||| ||||| ||||| |||||
Db 1339 AGTCATGACTGGAAAGATGGAGAAATCAAGGCTCCTTCAGGCCCC 1383
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RESULT 10
US-08-955-713-1/C
; Sequence 1, Application US/08955713
; Patent No. 5955308
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSMAN, DEBK-
; APPLICANT: HALSEY, WENDY

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1  APPLICANT: Brown, Michael S.
2  APPLICANT: Briggs, Michael R.
3  APPLICANT: Wang, Xiaodong
4  APPLICANT: Goldstein, Joseph L.
5  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
6  TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
7  TITLE OF INVENTION: PROTEINS
8  NUMBER OF SEQUENCES: 64
9  CORRESPONDENCE ADDRESS:
10 ADDRESSER: Arnold, White & Durkee
11 STREET: P.O. Box 4433
12 CITY: Houston
13 STATE: Texas
14 COUNTRY: U.S.A.
15 ZIP: 77210
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.30
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/131,365B
24 FILING DATE: 01-Oct-1993
25 CLASSIFICATION: 435
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Parker, David L.
28 REGISTRATION NUMBER: 32,165
29 REFERENCE/DOCKET NUMBER: UTSJ:372/PAR
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (512) 418-3000
32 TELEFAX: (512) 474-7577
33 INFORMATION FOR SEQ. ID NO: 37:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 4154 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: other nucleic acid
40 DESCRIPTION: /desc = "DNA"
41
42 FEATURE:
43 NAME/KEY: CDS
44 LOCATION: 167..3607
45
46 US-08-131-365B-37
47
48 Alignment Scores:
49 Pred. No.: 49 Length: 4154
50 Score: 66.00 Matches: 21
51 Percent Similarity: 47.62% Conservative: 9
52 Best local Similarity: 33.33% Mismatches: 23
53 Query Match: 14.83% Indels: 10
54 DB: 1 Gaps: 2
55
56 US-08-978-217-7 (1-84) x US-08-131-365B-37 (1-4154)
57
58 Oy 22 LeuARGAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeuLeuGlu 41
59 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 Db 1355 CTGAAGAGTCTGCGTGGCTGCGCTGTGCGACGTGAGGGAACACAGACTG---CTATGGAG 1411
61
62 Oy 42 LysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerPro 61
63 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 Db 1412 GGGCTGAAGACTGAGTGGAGGAGACACACTGACCCCACCCCCTCGGATCTGCTGCTACCT 1473
65
66 Oy 62 PheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyHisProGlySerCys 81
67 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
68 Db 1472 TTTCA-----CAGAGCAGCCCTTGTCTCCCTTGCGACAGG 1504
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70 Oy 82 GlyAlaGly 84
71 |||:|||||:
72 Db 1505 GGCAGTGAC 1513
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74 RESULT 12
75 US-08-668-123-37
76 / Sequence 37, Application US/08668123

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3546 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 2..2920
US-08-162-809-9

Alignment Scores:
Pred. No.: 63.3 Length: 3546
Score: 64.50 Matches: 22
Percent Similarity: 43.42% Conservative: 11
Best Local Similarity: 28.95% Mismatches: 38
Query Match: 14.49% Indels: 6
DB: 1 Gaps: 1

US-08-978-217-7 (1-84) x US-08-162-809-9 (1-3546)
QY 13 ProLeuGlyAAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerAAspGlu 32
DB 2170 CCTCTAGAGATGACTACCTGACCGAGACCTGG-CTGCCCGCAACATCTCTGTCACA 2228
QY 33 LeuSerTrpIleIleGluLeuLeuGluLyAspGlyMetAlaPheGlnGlnAlaLeuAsp 52
DB 2229 GCACTTGCTGTCGCAAGTCTGACTTCGGGCTCTCCGCTTTTGGAGGATGATCCAG 2288
QY 53 -----ProGlyProPheAspGlnGlySerProPheAlaGlnGluLeu 67
DB 2289 CCGACCCCACTACACAGCTCCCTGGGAGCAAGATCCCATCAGGTGACAGCTCTCG 2348
QY 68 AspAspGlyGlnGlnAlaSerProTrpHisProGlySerCyAspGlyAla 83
DB 2349 AGGCCATCGCTACCGCAATTCACTCGGCCAGCGAGCTGTGAGACT 2396

RESULT 15
US-08-162-809-13
Sequence 13, Application US/08162809
Patent No. 5457046
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoon G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3591 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 2..2965
US-08-162-809-13

Alignment Scores:
Pred. No.: 64.4 Length: 3591
Score: 64.50 Matches: 22
Percent Similarity: 43.42% Conservative: 11
Best Local Similarity: 28.95% Mismatches: 38
Query Match: 14.49% Indels: 6
DB: 1 Gaps: 1

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DB 2215 CCTCTAGAGATGACTACCTGACCGAGACCTGG-CTGCCCGCAACATCTCTGTCACA 2273
QY 33 LeuSerTrpIleIleGluLeuLeuGluLyAspGlyMetAlaPheGlnGlnAlaLeuAsp 52
DB 2274 GCACTTGCTGTCGCAAGTCTGACTTCGGGCTCTCCGCTTTTGGAGGATGATCCAG 2333
QY 53 -----ProGlyProPheAspGlnGlySerProPheAlaGlnGluLeu 67
DB 2334 CCGACCCCACTACACAGCTCCCTGGGAGCAAGATCCCATCAGGTGACAGCTCTCG 2393
QY 68 AspAspGlyGlnGlnAlaSerProTrpHisProGlySerCyAspGlyAla 83
DB 2394 AGGCCATCGCTACCGCAATTCACTCGGCCAGCGAGCTGTGAGACT 2441

Search completed: March 15, 2003, 23:33:00
Job time : 36.7601 secs

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